

Fig. 1

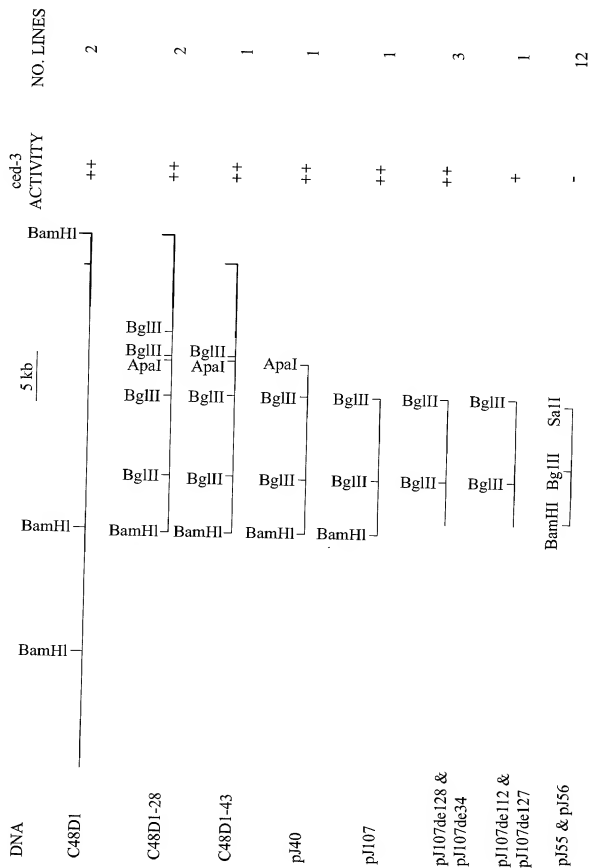


Fig. 2

ced-3 Genomic Sequence

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AGATCTGAAATAAGGTGATAAAATTAATAAAATTAAGTGATTTCTGAGGAAATTTGACTGT
1  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
TTTAGCACAAATTAATCTTGTTTCAGAAAAAAAGTCCAGTTTTCTAGATTTTCCCGTCTTA
61  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
TTGTCGAATTAATATCCCTATTATCACTTTTTCATGCTCATCTCCAGAGCGGCACGTCCTC
121  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
AAAGAAATGTGAGAGCAAAACGCGCTCCCATTGACCTCCCACTCAGCCGCCAAAAACAAC
181  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
GTTCGAACATTCGTGTGTTGTGCTCCTTTCCGTTATCTTCGAGTCATCTTTTGTGCGTT
241  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
TTTTCTTTGTTCTTTTGTGAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA
301  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
GGCTCGCCGATTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTATAATA
361  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTAACCTTGGTTTTTGTGATGTTTCGTTTAAAAAAACCACTGTTTATGTGAAAAACGA
421  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTTACCTCACCGCTCCGTTGTCATG
481  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
GCTCATAGATTTTCGATACTCAAATCCAAAAATAAATTACGAGGGCAATTAAATGTGAAA
541  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
CAAAAACAATCCTAAGATTTCCACATGTTTGACCTCTCCGGCACCTTCTTCCTTAGCCCC
601  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
ACCACCTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGTAT
661  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
CTCATTGTGATGCTCTTTTCGATTTTATAGCTCTTTGTGCAATTTCAATGCTTTAAAC
721  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 760
AATCCAAATCGCATTATATTGTGTCATGGAGGCAAAATGACGGGTTGGAATCTTAGATGA
781  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
GATCAGGAGCTTTCAGGGTAAACGCCCGGTTCAATTTGTACCACTTTCATCATTTTCCT
841  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
GTCGTCCTTGGTATCCTCAACTTGTCCCGGTTTGTGTTTCGGTCACTCTTCCGTGATGC
901  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
CACCTGTCTCCGTCTCAATTATCGTTTAGAAATGTGAACGTCCAGATGGGTGACTCATA
961  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
TTGCTGCTGCTACAATCCACTTTCTTTTCTCATCGGCAGTCTTACGAGCCCATCATAAAC
1021  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
TTTTTTTTCCCGGAAATTTGCAATAAACCGGCCAAAAAATTTCTCCAAATGTTACGCAA
1081  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
TATATACAATCCATAAGAAATATCTTCTCAATGTTTATGATTCTTCGAGCACTTTCTCT
1141  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
TCGTGTGCTAACATCTTATTTTATAATATTCCGCTAAAAATCCGATTTTGTAGTATTA
1201  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
ATTTATCGTAAATATCATAATAGCACCGAAAACTACTAAAAATGGTAAAAGCTCCTTT
1261  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320

Repeat 1
=====
TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATCTGAGAATGCGTACTGCGC
1321  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380

=====
AACATATTTGACGGCAAAAATATCTCGTAGCGAAAACTACAGTAATTCTTTAAATGACTAC
1381  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440

```

Fig. 3

```

                                     Repeat 1
=====> <=====
1441 TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTTGAAAAATAATTTTTTTTTTCGAATTT 1500
-----+-----+-----+-----+-----+
1501 TGATAACCCGTAATCGTCAACAACGCTACAGTAGTCATTTARAGGATTACTGTAGTTCTTA 1560
-----+-----+-----+-----+-----+
1561 GCTACGAGATATTTTGC GCGCCAAATATGACTGTAATACGCATTCTCTGAATTTTGTGTT 1620
-----+-----+-----+-----+-----+
1621 TCCGTAATAATTTCAACAAGATTTTGGCATTCCACTTTAAAGGCGCACAGGATTTATTCCA 1680
-----+-----+-----+-----+-----+
1681 ATGGGTCTCGGCACGCAAAAAGTTTGATAGACTTTTAAATTCTCCTTGCAATTTTAAATTC 1740
-----+-----+-----+-----+-----+
1741 AATTACTAAAATTTTCGTGAATTTTCTGTAAAAATTTTAAAAATCAGTTTCTCAATATT 1800
-----+-----+-----+-----+-----+
1801 TTCCAGGCTGACAAACAGAAACAAAAACACACAAACATTTTAAAAATCAGTTTTCAAAT 1860
-----+-----+-----+-----+-----+
1861 TAAAAATAACGATTTTCTCATTTGAAAATTGTGTTTTATGTTTGC GAAAAATAAAGAGAACT 1920
-----+-----+-----+-----+-----+
1921 GATTCAAAACAATTTTAACAAAAAAAACCCCAAAATTCGCCAGAAATCAAGATAAAAAA 1980
-----+-----+-----+-----+-----+
1981 TTCAAGAGGGTCAAAATTTTCCGATTTTACTGACTTTACCTTTTTCGTAAGTTCAAGT 2040
-----+-----+-----+-----+-----+
2041 GCAGTTGTTGGAGTTTTTGACGAAACTAGGAAAAAATCGATAAAAAATTACTCAAATCG 2100
-----+-----+-----+-----+-----+
2101 AGCTGAATTTTGAGGACAATGTTTAAAAAAAACACTATTTTCCAATAATTTCACTCAT 2160
-----+-----+-----+-----+-----+

-----
TTTCAGACTAAATCGAAAATCAAATCGTACTCTGACTACGGGTCAGTAGAGAGGTCAACC
-----
2161 -----+-----+-----+-----+-----+ 2220
2221 ATCAGCCGAAGATGATGCGTCAAGATAGAAGGAGCTTGCTAGAGAGGAACATTATGATGT 2280
-----+-----+-----+-----+-----+
          M M R Q D R R S L L E R N I M M F
          1                                10
                                T(n1040)
TCTCTAGTCATCTAAAAGTCGATGAAATTTCTCGAAGTTCTCATCGCAAAACAAGTGTGA
2281 -----+-----+-----+-----+-----+ 2340
          S S H L K V D E I L E V L I A K Q V L N
          20                                30
                                |intron 1
ATAGTGATAATGGAGATATGATTAATGTGAGTTTTTAAATCGAATAATAATTTTAAAAAAA
2341 -----+-----+-----+-----+-----+ 2400
          S D N G D M I N
          40
                                |
AATTGATAATATAAAGAATATTTTTCAGTCATGTGGAACGGTTTCGCGAGAAGAGACGGG
2401 -----+-----+-----+-----+-----+ 2460
                                S C G T V R E K R R E
                                50

```

Fig. 3 (cont.)

A (n718)

[illegible]

Fig. 3 (cont.)

030343-3

Fig. 3 (cont.)

4081 -----+-----+-----+-----+-----+ 4140
 TTTTTCGCAATTTTCTACATCACATGAATGTAGAAAATTAAAGGGAAATCAAAATTTCTA
 4141 -----+-----+-----+-----+-----+ 4200
 GAGGATATAATTGAATGAAACATTGCGAAATTAAAATGTGCGAAACGTCAAAAAAGAGGA
 4201 -----+-----+-----+-----+-----+ 4260

 AATTTGGGTATCAAAATCGATCCTAAAACCAACACATTTGAGCATCCGCCAACTCTTCAT
 4261 -----+-----+-----+-----+-----+ 4320
 S A N S S F
 180
 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTGAGCAAGCTT
 4321 -----+-----+-----+-----+-----+ 4380
 T G C S S L G Y S S S R N R S F S K A S
 190 200
 CTGGACCAACTCAATACATATTTCCATGAAGAGGATATGAACTTTGTGCGATGCACCAACCA
 4381 -----+-----+-----+-----+-----+ 4440
 G P T Q Y I F H E E D M N F V D A P T I
 210 220
 TAAGCCGTGTTTTCGACGAGAAAACCATGTACAGAACTTCTCGAGTCTCTGTTGAATGT
 4441 -----+-----+-----+-----+-----+ 4500
 S R V F D E K T M Y R N F S S P R G M C
 230 240
 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG
 4501 -----+-----+-----+-----+-----+ 4560
 L I I N N E H F E Q M P T R N N G T K A D
 250 260
 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA
 4561 -----+-----+-----+-----+-----+ 4620
 K D N L T N L F R C M G Y T V I C K D N
 270 280
 | intron 4
 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTTGCCATTTTGGC
 4621 -----+-----+-----+-----+-----+ 4680
 L T G R

 Repeat 3
 =====>
 CCGAAAAATGTGGCGCCCGTCTCGACACGACAAATTTGTGTTAAATGCAAAAATGTATAAT
 4681 -----+-----+-----+-----+-----+ 4740
 TTTGCAAAAAACAAAATTTTGAACCTCCGCGAAAAATGATTTACCTAGTTTCGAAATTTTC
 4741 -----+-----+-----+-----+-----+ 4800
 GTTTTTTCCGGCTACATTATGTGTTTTTTCTTAGTTTTCTATAATATTTGATGTAAAAA
 4801 -----+-----+-----+-----+-----+ 4860
 ACCGTTTGTAAATTTTCAGACAAATTTCCGCATACAAAACCTTGATAGCACGAAATCAATT
 4861 -----+-----+-----+-----+-----+ 4920
 TTCTGAATTTTCAAAATTTATCCAAAAATGCACAATTTAAAATTTGTGAAAAATGGCAAAAC
 4921 -----+-----+-----+-----+-----+ 4980

Fig. 3 (cont.)

086974-1

Fig. 3 (cont.)

Fig. 3 (cont.)

026824-3 0601

Repeat 5

=====

CTTGAACAACCAATGCGTGTCCTAAGTTTAAAGCACAGAAAAATAGCAGAGGGCTCCT
6541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6600

>

TTTTGCAAGCCGTGCCGCCTCAACTAGAATTITTAGTTTITAGCTAAAATGATTGATTTT
6601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6660

GAAATATTTTATGCTAAATTTTTTGGCGTTAAATTTTGAAATAGTCACATTTATCGGGTTT
6661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6720

CCAGTAATAAATGTTTATTAGCCATTGGATTITTAAGTAAACGAAAATTGTAGTTTTTC
6721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6780

AACGAAATTTATCGATTTTTTAAATGTAAAAAAAAATAGCGAAAATTACATCAACCATCAA
6781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6840

GCATTTAAGCCAATAATTTTAACTCATTTTAAATAATTAATTCAAAGTTGTCACGAGTATT
6841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6900

Repeat 5

<=====

ACACGGTTGGCGCGCGGAAGTTTGCAAACGACGCTCCGCCTCTTTTCTGTGCGGGTT
6901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6960

T(nl163)

=====
GAAACAAGGGATCGGTTTAGATTITCCCCAAAATTTAAATTAATTCAGATGACATC
6961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7020

M T S

CCGCCTGCTCAAAAAGTTCTACTTTTGGCCGAAGCAGAACTCTGCCGCTCAAAAATTC
7021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7080

R L L K F Y F W P E A R N S A V *

490 500

ACTCGTGATTCATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCAGTTCTCTTTGCG
7081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7140

CXAATAGTTTAAAAACATGTGTATTTGTATTCCTATACTCATTTCACTTTATCATTTCT
7141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7200

ATCATTTCTCTTCCCATTTCACACATTTCCATTTCTCTACGATAATCTAAAAATATGAC
7201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7260

GTTTGTGTCTCGAAGCATAATAATTTTAATAACTCGTTTTGAATTTGATTAGTTGTTGT
7261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7320

GCCAGTATATATGTATGCTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC
7321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7380

CCAACCCCAACCTACCGTACCATAATTCATTTTGGCCGGAATCAATTTTCGATTAATT
7381 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7440

TTAACCTATTTTTTGCCCAAAAAATCTAATATTTGAATTAACGAATAGCATTCACCATC
7441 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7500

TCCTCCGTGCGGAATGCTCCCGGCTTTTAAAGTTGGAACATTTGGCAATATGTAT
7501 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7560

AAATTTGTAGGTCCCCCATCATTTCCCGCCATCATCTCAAATTCGATTCTTTTTCG
7561 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7620

CGTGATATCCCGATTCTGGTCAGCAAGATCT

7621 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7653

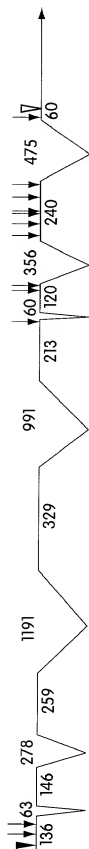


Fig. 4A

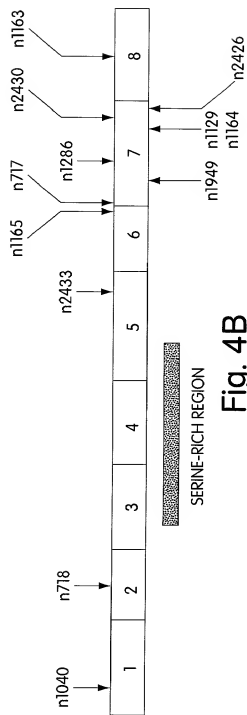


Fig. 4B

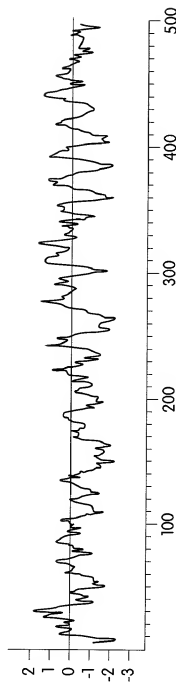


Fig. 5

Alignment of ced-3 and Human Interleukin -1 β convertase

```

ICE      1  MADKVLKEKRKLFIRSM...GEGTINGLLDELLQTRVLNKEEMKVKRE
          .: .:|. |: |: .: .: .: .: |: |. |: .: .: .
Ced-3    1  ...MMRQDRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMIN.S
                                     ↓
                                     F

BGAFQ
PBA

47  NATVMDKTRALIDSVIPKGAQACQ.ICITYICEEDSYLAGTLGLSADQTS
    :| |:| |:|. |:|. |:|. |:|. |:|. |:|. |:|. |:|. |:|.
47  CGTVREKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVD
                                     ↓
                                     R

BFAFQ
PBA

96  GNYLNMQ.....DSQGVLSST.....
    :| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
97  SNAVEFECPMSPASHRRSRALSPAGYTSPTRVHRDSVSSVSSTSYODIY
    serine-rich region

BGAFQ
PBA

112  .....PAPQAVQDNPMPTSSGSEGNVKLCSLE
     | :| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
147  SRARSRSRSLHSSDRHNYSSPPVNAFPOSSANSSTFTGCSSLGYSSS

BGAFQ
PBA

140  EAQRIWKQKSAEIYPIMDK.....SSRTRLAL
     .: .:|. |: |: .: .: .: .: |: |. |: .: .: |
197  RNRSFSKASGPTQYIFHEEDMNFVDAPTISR VFDEKTM YRNFSSPRGMCL

BGAFQ
PBA

```

Fig. 6A

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[illegible]

Fig. 6B

Alignment of N-terminal regions of ced-3/ICE-related proteins

c. briggsae ced-3	MWRQDRNSLLENTLFFSKQLADLLDLVLAKVQVLSNDGVNSCTTERDNEKEIVKAVVORGEAFDAFYDALRDTGHNDLADVPLSR---PNVF	100
ced-3 protein	MWRQDRNSLLENTLFFSKQLADLLDLVLAKVQVLSNDGVNSCTTERDNEKEIVKAVVORGEAFDAFYDALRDTGHNDLADVPLSR---PNVF	
C. vulgaris ced-3	MWRQDRNSLLENTLFFSKQLADLLDLVLAKVQVLSNDGVNSCTTERDNEKEIVKAVVORGEAFDAFYDALRDTGHNDLADVPLSR---PNVF	
Mouse ICE.gw	M-----ADKIL-----RAKRRQTFNSV-----SIGTINGILLDELLEK-----RVINQDEEM-----DKI	
Human ICE.gw	M-----ADKVL-----KEKKRLTIRSM-----GEGTINGILLDELLOQT-----RVINKEEM-----EKV	
Consensus	M.....AD IL.....V.....D.L.T.....VL.....	
c. briggsae ced-3	PMECPMSPHRRSRALSPGCIASPTVRHDSISVSSTFTQDYTSRARSRSRSPPLQSSDRHNYSIA--TSFPSPQSPSANSSTTCGASLGVSSSN	198
ced-3 protein	PMECPMSPHRRSRALSPGCIASPTVRHDSISVSSTFTQDYTSRARSRSRSPPLQSSDRHNYSIA--TSFPSPQSPSANSSTTCGASLGVSSSN	
C. vulgaris ced-3	PMECPMSPHRRSRALSPGCIASPTVRHDSISVSSTFTQDYTSRARSRSRSPPLQSSDRHNYSIA--TSFPSPQSPSANSSTTCGASLGVSSSN	
Mouse ICE.gw	KLA---NITAMDKARDLGDVHSKGPQASQIFTYICNEDCYL-----AGILLEQASPAE--TFVAT-----EDSKGCHHSSTSEKEQNKED-G	
Human ICE.gw	KKE---NATVMDKTRALIDSVTPKGAQACITTYICNEDSYL-----AGTIGLSADQTSG--NYIANN-----QDSQGVLSSTFPAPQAVQNPAMP	
Consensus	.E---.....RAL.....I.....SY.....S.SRS.R.L.SSDRHN.Y.S.-.-.F.SQP.SANSSTTG.-.SLGVSSSR.	
c. briggsae ced-3	RSFKTSASQVQIFHEEDMNVDAPTIHRVDEKTMVNFSSPRGCLITINNEHEFQMPTRNGTKAKONITWIFRCMGTVVIQDNLARGNLSLTIRSF	298
ced-3 protein	RSFKTSASQVQIFHEEDMNVDAPTIHRVDEKTMVNFSSPRGCLITINNEHEFQMPTRNGTKAKONITWIFRCMGTVVIQDNLARGNLSLTIRSF	
C. vulgaris ced-3	RSFKTSASQVQIFHEEDMNVDAPTIHRVDEKTMVNFSSPRGCLITINNEHEFQMPTRNGTKAKONITWIFRCMGTVVIQDNLARGNLSLTIRSF	
Mouse ICE.gw	TFPGLTGTLCFCPLEKAOAKWKNPS--EIV--PDAWT--TRTR--LALLICNTFFOLSPRVGAOVLREKILLDELGYVKKVENLTALEWVKEVSEF	
Human ICE.gw	TSSSGEGNWKLSLEAQRIRWQASA--EIV--PDAWS--SRTR--LALLICNEEDSIFPRVQGLVDITGHTWILLQNLGISVDVQVKQLTASMTTELEAF	
Consensus	RS.SK.S...QVIFHEEDMN.VDAPTI.RVDEKTMVNFSSPRGCLITINNEHEFQMPTRNGTK.IKDN.TWIFRCMGTVV.QDNLARGN.L.TIR.F	
c. briggsae ced-3	GRNDME--GDGAILVLISHGEENVILIG---VDDVS--VNVHEVYDLINMANAPRLANKPLVFFVQACRG	
ced-3 protein	GRNDME--GDGAILVLISHGEENVILIG---VDDVS--VNVHEVYDLINMANAPRLANKPLVFFVQACRG	
C. vulgaris ced-3	AKHESH--GDGAILVLISHGEENVILIG---VDDIP--ISVHEVYDLINMANAPRLANKPLVFFVQACRG	
Mouse ICE.gw	AKNETH--GDGAILVLISHGEENVILIG---VDDVS--VNVHEVYDLINMANAPRLANKPLVFFVQACRG	
Human ICE.gw	AACTPEHTSDSTFLVFNHSHGLREGIQSTTYNEVSDILKVDITPQANTFLNCSLKDKPRVLIITQACRG	
Consensus	AHRPEKTSDDSTFLVFNHSHGLREGTCKKHSEQVPDILQALNFTNCTNCPSLKKPKRVIIITQACRG	
Consensus	A...H...GDGAILVLISHGEENVILIG---VDDVS---VHEVYDLINMANAPRLANKPLVFFVQACRG	

Fig. 6C

Alignment of C-terminal regions of ced-3/ICE/NEDD-2 - related proteins

ICE C-terminus	DSGVW----	FDISVG----	-----V
Mouse ICE C-ter	EKGVL-----	LQSVR-----	-----D
C.briggsae C-ter	ERDNGFP-----	VLDSDG-----	-----RRGWN
ced-3 C-terminus	ERDNGFP-----	VLDSDG-----	-----VPSLI
C. vulgaria C-terminus	ERDVGFP-----	VLDSDG-----	-----VPAFL
nedd-2 protein.gw	MLVGVVTVTS	QKCSSEKHY	EYLLPPLT
Consensus	E.....	LDV..	-----P....
ICE C-terminus	SGNL---SLP	TTEEF---	D
Mouse ICE C-ter	SE-----DEL	TDALFE---	D
C.briggsae C-ter	RDG-PLFNF	LCVRPQV---	Q
ced-3 C-terminus	RDG-PLFNF	LCVRPQV---	Q
C. vulgaria C-terminus	GDG-P--NFL	LCVRPQV---	Q
nedd-2 protein.gw	QDGKHTQSP	GCESDAGK	ELMNLPT
Consensus	.DG---.FL	GC.....K..P..
ICE C-terminus	MSGVTFGLL	EHMQEVCSC	DVEIFRNV---
Mouse ICE C-ter	RGSLTFESLI	KHKKEYAWSC	DLEDIFRV---
C.briggsae C-ter	RGSLTFQAVC	EVFLHAKDM	DVELLTENV
ced-3 C-terminus	RGSLTFQAVC	EVFLHAKDM	DVELLTENV
C. vulgaria C-terminus	RGSLTFQAVC	EVFLHAKDM	DVELLTENV
nedd-2 protein.gw	RGSLTFQAVC	EVFLHAKDM	DVELLTENV
Consensus	RGSLTFQAVC	EVFLHAKDM	DVELLTENV
ICE C-terminus	T-ERYT-LZR	CFLLPFGH-----	
Mouse ICE C-ter	A-DRVT-LJK	RFLLPFGH-----	
C.briggsae C-ter	MPFLSRLLK	KFTFPEDRG	NSAV
ced-3 C-terminus	MPFLSRLLK	KFTFPEAR	NSAV
C. vulgaria C-terminus	MPFLSRLLK	KFTFPEARN	NSAV
nedd-2 protein.gw	MSGYCSLLQ	QLLPLFG-----	YPPT
Consensus	M.E..S.L.K	FL..E..	-----GF..

Fig. 6D

Lines

```

1 01 MMRQDRRSLERNIMMFSSHLKVDEILEVLIQVLSNDNGDMINSCGTV 50
2 .....W.....LE...K.QA.L..D.....V....R.E
3 TVSISLI..R..... M.....

1 51 REKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNAV 100
2 .DNEK.....R..E.....D...ND..D..M..S.P .P.
3

1 101 EFECMPSPASHRRSRALSPAGYTSPTRVHRDSVSSVSSFTS_YQDIYSRA 149
2 PM.....S.....P .A.....I.....T...V....
3 S

1 150 RSRSR_SRALHSSDRHNYSSPPVNAFSPQSSANSSTGCSSLGYSSSRN 198
2 ..S..S..P.Q.....M.AA_TS.....A.....
3 T..._.P..T.....V..S..S.Q...A.....S.....T

1 199 RSFSKASGPTQYIFHEEDMNFVDAPTISRVDKTMYNFSSPRGMCLI 247
2 .....T.AQS.....Y.....H.....L...
3 ..Y.....AHS.....Y.....H.....T...L...

1 248 INNEHFQOMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD 297
2 .....I.....E..S...S
3 .....P...IS.....I.H.....M.....

1 298 FAKHESHGDSAILVILSHGEENVIIIGVDDIPISTHEIYDLLNAANAPRLA 347
2 .GRNDM.....VSVNV.....
3 ...N.T.....VSVNV...x.....

1 348 NKPXKIVFVQACRGERRDNGFPVLDSVDGVPAFLRRGWDNDRGPLFNFLGC 397
2 ....L.....SLI.....
3 ....L.....V.....LI....KG...

1 398 VRPQVQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVEVFST 447
2 .....M..A.....L
3 ....A.....A.....L

1 448 HAKDMDVVVELLTEVNKKVACGFTSQGSNILKQMPEMTSRLKKFYFWPE 497
2 .....L.....
3 .....A.....L.....

1 498 __ARN__SAV 503
2 DRG.....
3 __D..RS...

```

Fig. 7

00888243.062201

Interleukin-1 β convertase cDNA sequence

1 AAAAGGAGAG AAAAGCCATG GCCGACAAGG TCCTGAAGGA GAAGAGAAAG
 51 CTGTTTATCC GTTCCATGGG TGAAGGTACA ATAAATGGCT TACTGGATGA
 101 ATTATTACAG ACAAGGGTGC TGAACAAGGA AGAGATGGAG AAAGTAAAC
 151 GTGAAATGC TACAGTTATG GATAAGACCC GAGCTTTGAT TGACTCCGTT
 201 ATTCCGAAAG GGGCACAGGC ATGCCAAATT TGCATCACAT ACATTTGTGA
 251 AGAAGACAGT TACCTGGCAG GGACGCTGGG ACTCTCAGCA GATCAAACAT
 301 CTGGAAATTA CCTTAATATG CAAGACTCTC AAGGAGTACT TTCTTCCTTT
 351 CCAGCTCCTC AGGCAGTGCA GGACAACCCA GCTATGCCCA CATCCTCAGG
 401 CTCAGAAGGG AATGTCAAGC TTTGCTCCCT AGAAGAAGCT CAAAGGATAT
 451 GGAACAACAAA GTCGGCAGAG ATTTATCCAA TAATGGACAA GTCAAGCCGC
 501 ACACGTCTTG CTCTCATTAT CTGCAATGAA GAATTTGACA GTATTCTTAG
 551 AAGAACTGGA GCTGAGGTTG ACATCACAGG CATGACAATG CTGCTACAAA
 601 ATCTGGGGTA CAGCGTAGAT GTGAAAAAAA ATCTCACTGC TTCGGACATG
 651 ACTACAGAGC TGGAGGCATT TGCACACCGC CCAGAGCACA AGACCTCTGA
 701 CAGCACGTTT CTGGTGTTCA TGTCTCATGG TATTCGGGAA GGCATTTTGT
 751 GGAAGAAAACA CTCTGAGCAA GTCCCAGATA TACTACAACT CAATGCAATC
 801 TTTAACATGT TGAATACCAA GAACTGCCCA AGTTTGAAGG ACAAAACCGAA
 851 GGTGATCATC ATCCAGGCCT GCCGTGGTGA CAGCCCTGGT GTGGTGTGGT
 901 TTAAGATTC AGTAGGAGTT TCTGGAAACC TATCTTTACC AACTACAGAA
 951 GAGTTTGAGG ATGATGCTAT TAAGAAAGCC CACATAGAGA AGGATTTTAT
 1001 CGCTTTCTGC TCTTCCACAC CAGATAATGT TTCTTGAGGA CATCCCACAA
 1051 TGGGCTCTGT TTTTATTGGA AGACTCATTG AACATATGCA AGAATATGCC
 1101 TGTTCCCTGTG ATGTGGAGGA AATTTTCCGC AAGGTTGAT TTTCAATTGA
 1151 GCAGCCAGAT GGTAGAGCGC AGATGCCAC CACTGAAAGA GTGACTTTGA
 1201 CAAGATGTTT CTACCTCTTC CCAGGACATT AAAATAAGGA AACTGTATGA
 1251 ATGTCTGCGG GCAGGAAAGT AAGAGATCGT TCTGTAAAAG GTTTTTGGAA
 1301 TTATGTCTGC TGAATAATAA ACTTTTTTTT AAATAATAAA TCTGGTAGAA
 1351 AAATGAAAAA AAAAAAAAAA AAA

Fig. 8

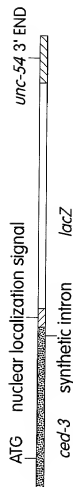
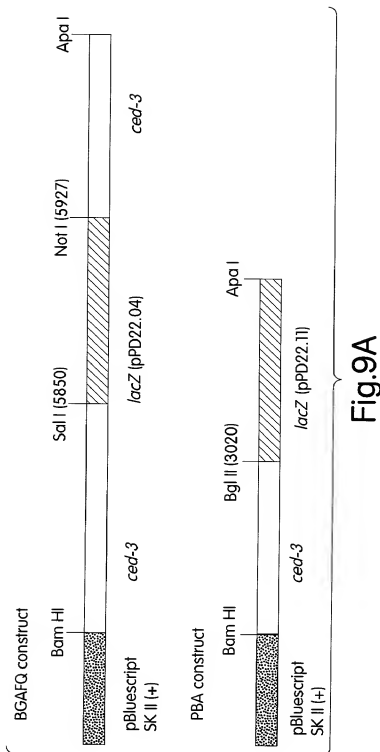


Fig.9B

20/24

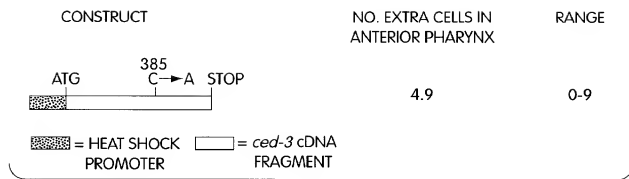


Fig. 10

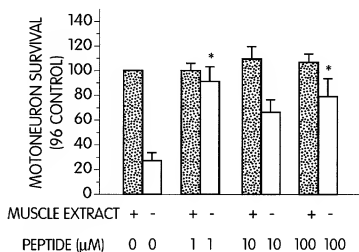


Fig. 11A

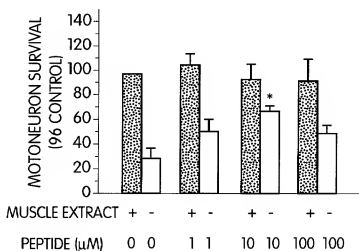


Fig. 11B

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21/24

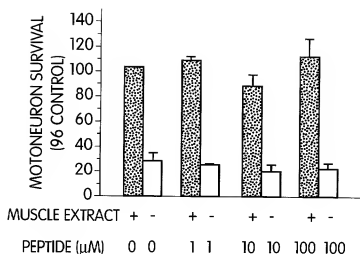


Fig. 11C

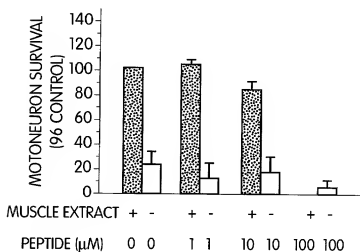


Fig. 11D

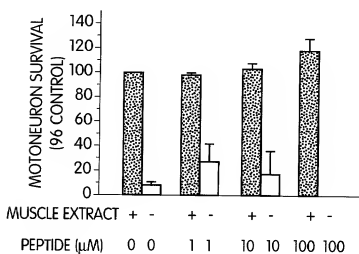
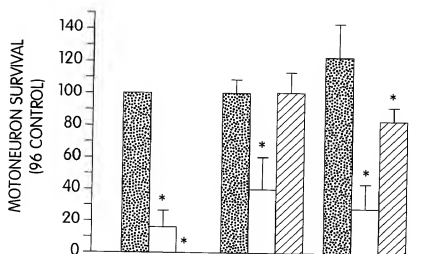
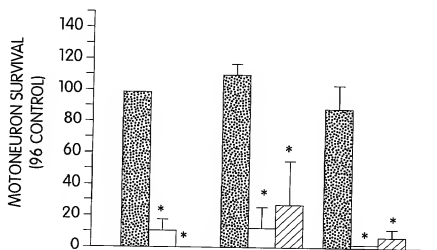


Fig. 11E



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12A



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12B

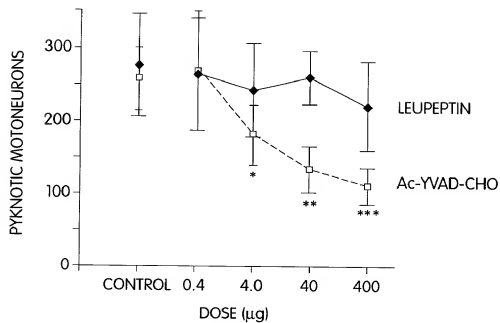


Fig. 13

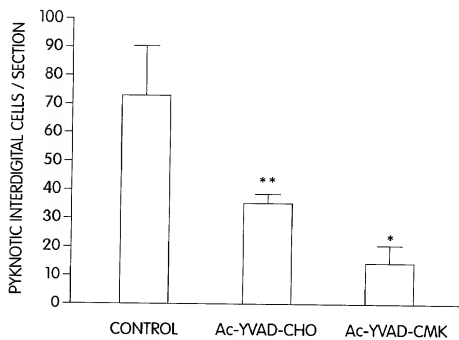


Fig. 14



Fig. 15C



Fig. 15D



Fig. 15E

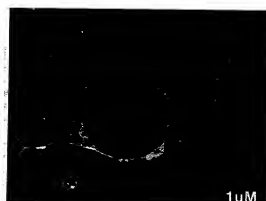


Fig. 15F



Fig. 15G